

#5



SEQUENCE LISTING

<110> Dhugga, Kanwarpal S.

<120> Manipulation of Sucrose Synthase Genes
to Improve Stalk and Grain Quality

<130> 1301P

<140> US 10/080,114

<141> 2002-02-21

<150> US 60/270,777

<151> 2001-02-22

<160> 13

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Zea mays

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<212> PRT

<213> Zea mays

<400> 2

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Gly	Ile	Leu	Gln	Pro	His	His	Ile	Leu	Asp	Ala	Leu	Asp	Glu	Val	Gln
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Gly	Ser	Gly	Gly	Arg	Ala	Leu	Ala	Glu	Gly	Pro	Phe	Leu	Asp	Val	Leu
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Arg	Ser	Ala	Gln	Glu	Ala	Ile	Val	Leu	Pro	Pro	Phe	Val	Ala	Ile	Ala
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Val	Arg	Pro	Arg	Pro	Gly	Val	Trp	Glu	Tyr	Val	Arg	Val	Asn	Val	His
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Glu	Glu	Leu	Val	Asp	Gly	Gln	His	Asn	Asp	Pro	Tyr	Val	Leu	Glu	Leu
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Asp	Phe	Glu	Pro	Phe	Asn	Val	Ser	Val	Pro	Arg	Pro	Asn	Arg	Ser	Ser
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Met	Phe	Arg	Asn	Arg	Asp	Cys	Leu	Glu	Pro	Leu	Leu	Asp	Phe	Leu	Arg
				165					170					175	
Gly	His	Arg	His	Lys	Gly	His	Val	Met	Met	Leu	Asn	Asp	Arg	Ile	Gln
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Ser	Leu	Gly	Arg	Leu	Gln	Ser	Val	Leu	Thr	Lys	Ala	Glu	Glu	His	Leu
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Ser	Lys	Leu	Pro	Ala	Asp	Thr	Pro	Tyr	Ser	Gln	Phe	Ala	Tyr	Lys	Phe
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Gln	Glu	Trp	Gly	Leu	Glu	Lys	Gly	Trp	Gly	Asp	Thr	Ala	Gly	His	Val
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Leu	Glu	Met	Ile	His	Leu	Leu	Leu	Asp	Ile	Ile	Gln	Ala	Pro	Asp	Pro
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Leu	Pro	Asp	Thr	Gly	Gly	Gln	Ile	Val	Tyr	Ile	Leu	Asp	Gln	Val	Arg
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Ala	Leu	Glu	Asn	Glu	Met	Val	Leu	Arg	Leu	Lys	Lys	Gln	Gly	Leu	Asp
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Val	Ser	Pro	Lys	Ile	Leu	Ile	Val	Thr	Arg	Leu	Ile	Pro	Asp	Ala	Lys
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Gly	Thr	Ser	Cys	Asn	Gln	Arg	Leu	Glu	Arg	Ile	Ser	Gly	Thr	Gln	His
		340						345					350		
Thr	Tyr	Ile	Leu	Arg	Val	Pro	Phe	Arg	Asn	Glu	Asn	Gly	Ile	Leu	Lys
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Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp	Pro	Tyr	Leu	Glu	Thr	Phe	Ala
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Glu	Asp	Ala	Ala	Gly	Glu	Ile	Ala	Ala	Glu	Leu	Gln	Gly	Thr	Pro	Asp
385					390					395					400
Phe	Ile	Ile	Gly	Asn	Tyr	Ser	Asp	Gly	Asn	Leu	Val	Ala	Ser	Leu	Leu
				405					410					415	
Ser	Tyr	Lys	Met	Gly	Ile	Thr	Gln	Cys	Asn	Ile	Ala	His	Ala	Leu	Glu
			420					425					430		
Lys	Thr	Lys	Tyr	Pro	Asp	Ser	Asp	Ile	Phe	Trp	Lys	Asn	Phe	Asp	Glu
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Asn Ala Asp Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Ser					
465		470		475	480
Lys Asn Thr Val Gly Gln Tyr Glu Ser His Thr Ala Phe Thr Leu Pro					
	485		490		495
Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe					
	500		505		510
Asn Ile Val Ser Pro Gly Ala Asp Met Ser Ile Tyr Phe Pro His Thr					
	515		520		525
Glu Lys Ala Lys Arg Leu Thr Ser Leu His Gly Ser Ile Glu Asn Leu					
	530		535		540
Ile Tyr Asp Pro Glu Gln Asn Asp Glu His Ile Gly His Leu Asp Asp					
545		550		555	560
Arg Ser Lys Pro Ile Leu Phe Ser Met Ala Arg Leu Asp Arg Val Lys					
	565		570		575
Asn Ile Thr Gly Leu Val Glu Ala Phe Ala Lys Cys Ala Lys Leu Arg					
	580		585		590
Glu Leu Val Asn Leu Val Val Val Ala Gly Tyr Asn Asp Val Asn Lys					
	595		600		605
Ser Lys Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Met His Glu Leu					
	610		615		620
Ile Lys Thr His Asn Leu Phe Gly Gln Phe Arg Trp Ile Ser Ala Gln					
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Thr Asn Arg Ala Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr					
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His Gly Ala Phe Val Gln Pro Ala Leu Tyr Glu Ala Phe Gly Leu Thr					
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Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Leu His					
	675		680		685
Gly Gly Pro Ala Glu Ile Ile Glu His Gly Val Ser Gly Phe His Ile					
	690		695		700
Asp Pro Tyr His Pro Glu Gln Ala Val Asn Leu Met Ala Asp Phe Phe					
705		710		715	720
Asp Arg Cys Lys Gln Asp Pro Asp His Trp Val Asn Ile Ser Gly Ala					
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Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Ile Tyr Ser Glu					
	740		745		750
Arg Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser					
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Lys Leu Glu Arg Leu Glu Thr Arg Arg Tyr Leu Glu Met Phe Tyr Ile					
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785		790		795	800
Pro Gln					

<210> 3

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based upon the adapter
sequence and poly T to remove clones which have a
poly A tail but no cDNA.

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36

<210> 4

<211> 2746

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (72)...(2480)

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Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu

1

5

10

cgc ctt ggt gcc acc ttc tcc tcc cat ccc aat gaa ctg ata gca ctc 158

Arg Leu Gly Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu

15

20

25

ttt tcc agg tat gtt cac cag ggc aag gga atg ctt cag cgc cat cag 206

Phe Ser Arg Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln

30	35	40	45	
ctg ctt gcg gag ttt gat gcc ctg ttt gat agt gac aag gag aag tat				254
Leu Leu Ala Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr				
	50	55	60	
gca cca ttt gaa gac att ctt cgt gct gct cag gaa gca att gtg ctc				302
Ala Pro Phe Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu				
	65	70	75	
ccc cca tgg gtt gca ctt gct atc agg cca agg cct ggt gtc tgg gat				350
Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp				
	80	85	90	
tac att cgg gtg aat gta agt gag ctg gct gtg gag gag ctg agt gtt				398
Tyr Ile Arg Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Ser Val				
	95	100	105	
tct gag tac ttg gca ttc aag gaa cag ctg gtg gat gga caa tcc aac				446
Ser Glu Tyr Leu Ala Phe Lys Glu Gln Leu Val Asp Gly Gln Ser Asn				
110	115	120	125	
agc aac ttt gtg ctt gag ctt gat ttt gag ccc ttc aat gcc tcc ttt				494
Ser Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe				
	130	135	140	
cct cgt cct tcc atg tcg aag tcc atc gga aat gga gtg caa ttc ctt				542
Pro Arg Pro Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu				
	145	150	155	

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Asn Arg His Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr	
160 165 170	
ccc ttg ctg aac ttc ctc aag gct cat aac tac aag ggc acg acg atg	638
Pro Leu Leu Asn Phe Leu Lys Ala His Asn Tyr Lys Gly Thr Thr Met	
175 180 185	
atg ttg aat gac aga atc caa agc ctt cgt ggt ctc caa tca tcc ctg	686
Met Leu Asn Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ser Leu	
190 195 200 205	
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Arg Lys Ala Glu Glu Tyr Leu Leu Ser Val Pro Gln Asp Thr Pro Tyr	
210 215 220	
tcg gag ttc aac cat agg ttc caa gag ctt ggc ttg gag aag ggt tgg	782
Ser Glu Phe Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp	
225 230 235	
ggc gac act gcg aag cgt gtt ctc gac aca ctc cac ttg ctt ctc gac	830
Gly Asp Thr Ala Lys Arg Val Leu Asp Thr Leu His Leu Leu Leu Asp	
240 245 250	
ctt ctt gag gcc cct gat cct gcc aac ttg gag aag ttc ctt gga act	878
Leu Leu Glu Ala Pro Asp Pro Ala Asn Leu Glu Lys Phe Leu Gly Thr	
255 260 265	

ata cca atg atg ttc aac gtt gtt atc ctg tct cct cat ggc tac ttc 926
Ile Pro Met Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe
270 275 280 285

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Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg	
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	315

agg ctg ttg cct gat gct gct ggg act acg tgc ggt cag cgg ctg gag 1118
Arg Leu Leu Pro Asp Ala Ala Gly Thr Thr Cys Gly Gln Arg Leu Glu
335 340 345

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Asn Glu Asn Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp
370 375 380

Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ser Ser Glu Ile Met Lys	
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gaa atg cag gcc aag cct gac ctt atc att ggc aac tac agc gat ggc	1310
Glu Met Gln Ala Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly	
400	405
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aac cta gtc gcc act ctg ctc gcg cac aag ttg gga gtc act cag tgt	1358
Asn Leu Val Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys	
415	420
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acc atc gct cat gcc ttg gag aaa acc aaa tac ccc aac tcg gac atc	1406
Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile	
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440	445
tac ttg gac aaa ttc gac agc cag tac cac ttc tct tgc cag ttc aca	1454
Tyr Leu Asp Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr	
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gct gac ctt att gcc atg aac cac acc gat ttc atc atc acc agc aca	1502
Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr	
465	470
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ttc caa gaa atc gcg gga agc aag gac acc gtg ggg cag tac gag tcc	1550
Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu Ser	
480	485
490	
cat atc gcg ttc act ctt cct ggg ctc tac cgt gtc gtc cat ggc atc	1598
His Ile Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile	

495	500	505	
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Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met			
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Ser Val Tyr Tyr Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe			
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cat cct gaa atc gag gag ctc atc tac agc gac gtc gag aac tcc gag			1742
His Pro Glu Ile Glu Glu Leu Ile Tyr Ser Asp Val Glu Asn Ser Glu			
	545	550	555
cac aag ttc gtg ctg aag gac aag aag aag ccg atc atc ttc tcg atg			1790
His Lys Phe Val Leu Lys Asp Lys Lys Lys Pro Ile Ile Phe Ser Met			
	560	565	570
gcg cgt ctc gac cgc gtg aag aac atg aca ggc ctg gtc gag atg tac			1838
Ala Arg Leu Asp Arg Val Lys Asn Met Thr Gly Leu Val Glu Met Tyr			
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ggc aag aac gcg cgc ctg agg gag ctg gcg aac ctc gtg atc gtt gcc			1886
Gly Lys Asn Ala Arg Leu Arg Glu Leu Ala Asn Leu Val Ile Val Ala			
590	595	600	605
ggc gac cac ggc aag gag tcc aag gac agg gag gag cag gcg gag ttc			1934
Gly Asp His Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe			
	610	615	620

aag aag atg tac agc ctc atc gac gag tac aag ttg aag ggc cat atc	1982
Lys Lys Met Tyr Ser Leu Ile Asp Glu Tyr Lys Leu Lys Gly His Ile	
625 630 635	
cgg tgg atc tcg gcg cag atg aac cgt gtc cgc aac ggg gag ctg tac	2030
Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr	
640 645 650	
cgc tac att tgc gat acc aag ggc gca ttc gtg cag cct gcg ttc tac	2078
Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr	
655 660 665	
gaa gcg ttc ggc ctg act gtg atc gag tcc atg acg tgc ggt ctg cca	2126
Glu Ala Phe Gly Leu Thr Val Ile Glu Ser Met Thr Cys Gly Leu Pro	
670 675 680 685	
acg atc gcg acc tgc cat ggc ggc cct gct gag atc atc gtg gac ggg	2174
Thr Ile Ala Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asp Gly	
690 695 700	
gta tct ggc ctg cac att gac cct tac cac agc gac aag gcc gcg gat	2222
Val Ser Gly Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp	
705 710 715	
atc ctg gtc aac ttc ttt gac aaa tgc aag gca gat ccg agc tac tgg	2270
Ile Leu Val Asn Phe Phe Asp Lys Cys Lys Ala Asp Pro Ser Tyr Trp	
720 725 730	

gac gag atc tca cag ggc ggc ctg cag aga att tat gag aag tac acc 2318
 Asp Glu Ile Ser Gln Gly Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr

735

740

745

tgg aag ctc tac tcc gag agg ctg atg acc ctg acc ggc gtg tac ggg 2366
 Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly

750

755

760

765

ttc tgg aag tac gtg agc aac ctg gag agg cgc gag acc cgc cgc tac 2414
 Phe Trp Lys Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr

770

775

780

atc gag atg ttc tac gcc ctg aag tac cgt agc ctg gca agc cag gtt 2462
 Ile Glu Met Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ser Gln Val

785

790

795

ccg ctg tcc ttc gat tag tacggggaaa gaaggagaag aagaagaaga 2510
 Pro Leu Ser Phe Asp *

800

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agtcgtgtat tggagttatg tgtacttggt ttccaagaac tttggttcct tctcgttttt 2630

tttccttggt tgagcgtttt tgggcagcgc tggcctgggt cctagtatgg tgggaattgg 2690

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<212> PRT

<213> Zea mays

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Tyr	Val	His	Gln	Gly	Lys	Gly	Met	Leu	Gln	Arg	His	Gln	Leu	Leu	Ala
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Glu	Phe	Asp	Ala	Leu	Phe	Asp	Ser	Asp	Lys	Glu	Lys	Tyr	Ala	Pro	Phe
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Glu	Asp	Ile	Leu	Arg	Ala	Gln	Glu	Ala	Ile	Val	Leu	Pro	Pro	Trp	
65					70				75					80	
Val	Ala	Leu	Ala	Ile	Arg	Pro	Arg	Pro	Gly	Val	Trp	Asp	Tyr	Ile	Arg
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Val	Asn	Val	Ser	Glu	Leu	Ala	Val	Glu	Glu	Leu	Ser	Val	Ser	Glu	Tyr
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Leu	Ala	Phe	Lys	Glu	Gln	Leu	Val	Asp	Gly	Gln	Ser	Asn	Ser	Asn	Phe
		115					120					125			
Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Ala	Ser	Phe	Pro	Arg	Pro
	130					135					140				
Ser	Met	Ser	Lys	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu	Asn	Arg	His
145					150					155				160	
Leu	Ser	Ser	Lys	Leu	Phe	Gln	Asp	Lys	Glu	Ser	Leu	Tyr	Pro	Leu	Leu
				165					170					175	
Asn	Phe	Leu	Lys	Ala	His	Asn	Tyr	Lys	Gly	Thr	Thr	Met	Met	Leu	Asn
			180					185					190		
Asp	Arg	Ile	Gln	Ser	Leu	Arg	Gly	Leu	Gln	Ser	Ser	Leu	Arg	Lys	Ala
		195					200					205			
Glu	Glu	Tyr	Leu	Leu	Ser	Val	Pro	Gln	Asp	Thr	Pro	Tyr	Ser	Glu	Phe
	210					215					220				
Asn	His	Arg	Phe	Gln	Glu	Leu	Gly	Leu	Glu	Lys	Gly	Trp	Gly	Asp	Thr
225					230					235				240	
Ala	Lys	Arg	Val	Leu	Asp	Thr	Leu	His	Leu	Leu	Leu	Asp	Leu	Leu	Glu
				245					250					255	
Ala	Pro	Asp	Pro	Ala	Asn	Leu	Glu	Lys	Phe	Leu	Gly	Thr	Ile	Pro	Met
			260					265					270		
Met	Phe	Asn	Val	Val	Ile	Leu	Ser	Pro	His	Gly	Tyr	Phe	Ala	Gln	Ser
	275					280						285			
Asn	Val	Leu	Gly	Tyr	Pro	Asp	Thr	Gly	Gly	Gln	Val	Val	Tyr	Ile	Leu
	290					295					300				
Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Leu	Leu	Arg	Ile	Lys	Gln
305					310					315				320	
Gln	Gly	Leu	Asp	Ile	Thr	Pro	Lys	Ile	Leu	Ile	Val	Thr	Arg	Leu	Leu
				325					330					335	
Pro	Asp	Ala	Ala	Gly	Thr	Thr	Cys	Gly	Gln	Arg	Leu	Glu	Lys	Val	Ile
			340					345					350		
Gly	Thr	Glu	His	Thr	Asp	Ile	Ile	Arg	Val	Pro	Phe	Arg	Asn	Glu	Asn
	355					360						365			
Gly	Ile	Leu	Arg	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp	Pro	Tyr	Leu
	370					375					380				
Glu	Thr	Tyr	Thr	Glu	Asp	Val	Ser	Ser	Glu	Ile	Met	Lys	Glu	Met	Gln
385					390					395				400	
Ala	Lys	Pro	Asp	Leu	Ile	Ile	Gly	Asn	Tyr	Ser	Asp	Gly	Asn	Leu	Val
				405					410					415	
Ala	Thr	Leu	Leu	Ala	His	Lys	Leu	Gly	Val	Thr	Gln	Cys	Thr	Ile	Ala

<213> Zea mays

<220>

<221> CDS

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Met Gly Glu Gly Ala Gly Asp Arg Val

1

5

ctg agc cgc ctc cac agc gtc agg gag cgc att ggc gac tca ctc tct 102

Leu Ser Arg Leu His Ser Val Arg Glu Arg Ile Gly Asp Ser Leu Ser

10

15

20

25

gcc cac ccc aat gag ctt gtc gcc gtc ttc acc agg ctg aaa aac ctt 150

Ala His Pro Asn Glu Leu Val Ala Val Phe Thr Arg Leu Lys Asn Leu

30

35

40

gga aag ggt atg ctg cag ccc cac cag atc att gcc gag tac aac aat 198

Gly Lys Gly Met Leu Gln Pro His Gln Ile Ile Ala Glu Tyr Asn Asn

45

50

55

gcg atc cct gag gct gag cgc gag aag ctc aag gat ggt gct ttt gag 246

Ala Ile Pro Glu Ala Glu Arg Glu Lys Leu Lys Asp Gly Ala Phe Glu

60

65

70

gat gtc ctg agg gca gct cag gag gcg att gtc atc ccc cca tgg gtt 294

Asp Val Leu Arg Ala Ala Gln Glu Ala Ile Val Ile Pro Pro Trp Val

75	80	85	
gca ctt gcc atc cgc cct agg cct ggt gtc tgg gag tat gtg agg gtc			342
Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Val			
90	95	100	105
aac gtc agt gag ctc gct gtt gag gag ctg aga gtt cct gag tac ctg			390
Asn Val Ser Glu Leu Ala Val Glu Glu Leu Arg Val Pro Glu Tyr Leu			
	110	115	120
cag ttc aag gaa cag ctt gtg gaa gaa ggc ccc aac aac aac ttt gtt			438
Gln Phe Lys Glu Gln Leu Val Glu Glu Gly Pro Asn Asn Asn Phe Val			
	125	130	135
ctt gag ctg gac ttt gag cca ttc aat gcc tcc ttc ccc cgt cct tct			486
Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro Ser			
	140	145	150
ctg tca aag tcc att ggc aat ggc gtg cag ttc ctc aac agg cac ctg			534
Leu Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu			
	155	160	165
tca tca aag ctc ttc cat gac aag gag agc atg tac ccc ttg ctc aac			582
Ser Ser Lys Leu Phe His Asp Lys Glu Ser Met Tyr Pro Leu Leu Asn			
170	175	180	185
ttc ctt cgc gcc cac aac tac aag ggg atg acc atg atg ttg aac gac			630
Phe Leu Arg Ala His Asn Tyr Lys Gly Met Thr Met Met Leu Asn Asp			
	190	195	200

aga atc cgc agt ctc agt gct ctg caa ggt gcg ctg agg aag gct gag	678
Arg Ile Arg Ser Leu Ser Ala Leu Gln Gly Ala Leu Arg Lys Ala Glu	
205 210 215	
 gag cac ctg tcc acc cta caa gct gat acc cca tac tct gaa ttt cac	726
Glu His Leu Ser Thr Leu Gln Ala Asp Thr Pro Tyr Ser Glu Phe His	
220 225 230	
 cac agg ttc cag gaa ctt ggt ctg gag aag ggt tgg ggt gat tgc gct	774
His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Cys Ala	
235 240 245	
 aag cgt gca cag gag act atc cac ctc ctc ttg gac ctc ctg gag gcc	822
Lys Arg Ala Gln Glu Thr Ile His Leu Leu Leu Asp Leu Leu Glu Ala	
250 255 260 265	
 cca gat ccg tcc acc ctg gag aag ttc ctt gga acg atc ccc atg gtg	870
Pro Asp Pro Ser Thr Leu Glu Lys Phe Leu Gly Thr Ile Pro Met Val	
270 275 280	
 ttc aat gtc gtt atc ctc tcc cct cat ggt tac ttc gct caa gct aat	918
Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ala Asn	
285 290 295	
 gtc ttg ggt tac cct gac acc gga ggc cag gtt gtc tac atc ttg gat	966
Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu Asp	
300 305 310	

caa gtg cgc gct atg gag aac gaa atg ctg ctg agg atc aag cag tgt	1014
Gln Val Arg Ala Met Glu Asn Glu Met Leu Leu Arg Ile Lys Gln Cys	
315 320 325	
ggg ctt gac atc acg ccg aag atc ctt att gtc acc agg ttg ctc cct	1062
Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu Pro	
330 335 340 345	
gat gca act ggc acc acc tgt ggc cag cgc ctt gag aag gtc ctt ggc	1110
Asp Ala Thr Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Leu Gly	
350 355 360	
acc gag cac tgc cat atc ctt cgc gtg cca ttc aga aca gaa aac gga	1158
Thr Glu His Cys His Ile Leu Arg Val Pro Phe Arg Thr Glu Asn Gly	
365 370 375	
atc gtt cgc aag tgg atc tcg cga ttt gaa gtc tgg ccg tac ctg gag	1206
Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Val Trp Pro Tyr Leu Glu	
380 385 390	
act tac act gat gac gtg gcg cat gag att gct gga gag ctt cag gcc	1254
Thr Tyr Thr Asp Asp Val Ala His Glu Ile Ala Gly Glu Leu Gln Ala	
395 400 405	
aat cct gac ctg atc atc gga aac tac agt gac gga aac ctt gtt gcg	1302
Asn Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala	
410 415 420 425	
tgt ttg ctc gcc cac aag atg ggt gtt act cac tgt acc att gcc cat	1350

540	545	550	
gag gag ctc ctg tac agc caa acc gag aac acg gag cac aag ttc gtt			1734
Glu Glu Leu Leu Tyr Ser Gln Thr Glu Asn Thr Glu His Lys Phe Val			
555	560	565	
ctg aac gac agg aac aag cca atc atc ttc tcc atg gct cgt ctc gac			1782
Leu Asn Asp Arg Asn Lys Pro Ile Ile Phe Ser Met Ala Arg Leu Asp			
570	575	580	585
cgt gtg aag aac ttg act ggg ctg gtg gag ctg tac ggc cgg aac aag			1830
Arg Val Lys Asn Leu Thr Gly Leu Val Glu Leu Tyr Gly Arg Asn Lys			
	590	595	600
cgg ctg cag gag ctg gtg aac ctc gtg gtc gtc tgc ggc gac cat ggc			1878
Arg Leu Gln Glu Leu Val Asn Leu Val Val Val Cys Gly Asp His Gly			
605	610	615	
aac cct tcc aag gac aag gag gag cag gcc gag ttc aag aag atg ttt			1926
Asn Pro Ser Lys Asp Lys Glu Glu Gln Ala Glu Phe Lys Lys Met Phe			
620	625	630	
gac ctc atc gag cag tac aac ctg aac ggg cac atc cgc tgg atc tcc			1974
Asp Leu Ile Glu Gln Tyr Asn Leu Asn Gly His Ile Arg Trp Ile Ser			
635	640	645	
gcc cag atg aac cgc gtc cgc aac ggc gag ctg tac cgc tac atc tgc			2022
Ala Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Cys			
650	655	660	665

gac acc aag ggc gcc ttc gtg cag cct gct ttc tac gag gct ttc ggg	2070
Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe Gly	
670 675 680	
ctg acg gtg gtt gag gcc atg acc tgc ggc ctg ccc acg ttc gcc acc	2118
Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr	
685 690 695	
gcc tac ggc ggt ccg gcc gag atc atc gtg cac ggc gtg tct ggc tac	2166
Ala Tyr Gly Gly Pro Ala Glu Ile Ile Val His Gly Val Ser Gly Tyr	
700 705 710	
cac atc gac cct tac cag ggc gac aag gcg tcg gcc ctg ctc gtg gac	2214
His Ile Asp Pro Tyr Gln Gly Asp Lys Ala Ser Ala Leu Leu Val Asp	
715 720 725	
ttc ttc gac aag tgc cag gcg gag ccg agc cac tgg agc aag atc tcc	2262
Phe Phe Asp Lys Cys Gln Ala Glu Pro Ser His Trp Ser Lys Ile Ser	
730 735 740 745	
cag ggc ggg ctc cag cgt atc gag gag aag tac acc tgg aag ctg tac	2310
Gln Gly Gly Leu Gln Arg Ile Glu Glu Lys Tyr Thr Trp Lys Leu Tyr	
750 755 760	
tcg gag agg ctg atg acc ctc acc ggc gtg tac ggg ttc tgg aag tac	2358
Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys Tyr	
765 770 775	

gtg tcc aac ctg gag agg cgc gag acc cgg cgg tac ctg gag atg ctg 2406
 Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met Leu

780 785 790

tac gcg ctc aag tac cgc acc atg gcg agc acc gtg ccg ctg gcc gtg 2454
 Tyr Ala Leu Lys Tyr Arg Thr Met Ala Ser Thr Val Pro Leu Ala Val

795 800 805

gag gga gag ccc tcc agc aag tga tgcgtgacgg cggccacaga cctgatcgat 2508
 Glu Gly Glu Pro Ser Ser Lys *

810 815

cgatgagcga gagggagcac tcggagtgtc gtgtcttttc ccttgccatt tctttctttc 2568
 ttctttttcc ttcccgagg cgaaaaaaaa agagtctgct ttgctaggc ggcgggcgtt 2628
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<211> 816

<212> PRT

<213> Zea mays

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 Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Pro Asn Glu Leu Val
 20 25 30
 Ala Val Phe Thr Arg Leu Lys Asn Leu Gly Lys Gly Met Leu Gln Pro

			500					505					510				
Val	Val	His	Gly	Ile	Asp	Val	Phe	Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser		
		515					520					525					
Pro	Gly	Ala	Asp	Leu	Ser	Ile	Tyr	Phe	Pro	Tyr	Thr	Glu	Ser	His	Lys		
	530					535					540						
Arg	Leu	Thr	Ser	Leu	His	Pro	Glu	Ile	Glu	Glu	Leu	Leu	Tyr	Ser	Gln		
545					550					555					560		
Thr	Glu	Asn	Thr	Glu	His	Lys	Phe	Val	Leu	Asn	Asp	Arg	Asn	Lys	Pro		
				565					570					575			
Ile	Ile	Phe	Ser	Met	Ala	Arg	Leu	Asp	Arg	Val	Lys	Asn	Leu	Thr	Gly		
		580					585					590					
Leu	Val	Glu	Leu	Tyr	Gly	Arg	Asn	Lys	Arg	Leu	Gln	Glu	Leu	Val	Asn		
	595						600				605						
Leu	Val	Val	Val	Cys	Gly	Asp	His	Gly	Asn	Pro	Ser	Lys	Asp	Lys	Glu		
	610						615				620						
Glu	Gln	Ala	Glu	Phe	Lys	Lys	Met	Phe	Asp	Leu	Ile	Glu	Gln	Tyr	Asn		
625					630					635					640		
Leu	Asn	Gly	His	Ile	Arg	Trp	Ile	Ser	Ala	Gln	Met	Asn	Arg	Val	Arg		
				645					650					655			
Asn	Gly	Glu	Leu	Tyr	Arg	Tyr	Ile	Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val		
			660					665					670				
Gln	Pro	Ala	Phe	Tyr	Glu	Ala	Phe	Gly	Leu	Thr	Val	Val	Glu	Ala	Met		
	675						680					685					
Thr	Cys	Gly	Leu	Pro	Thr	Phe	Ala	Thr	Ala	Tyr	Gly	Gly	Pro	Ala	Glu		
	690					695				700							
Ile	Ile	Val	His	Gly	Val	Ser	Gly	Tyr	His	Ile	Asp	Pro	Tyr	Gln	Gly		
705					710					715					720		
Asp	Lys	Ala	Ser	Ala	Leu	Leu	Val	Asp	Phe	Phe	Asp	Lys	Cys	Gln	Ala		
				725					730					735			
Glu	Pro	Ser	His	Trp	Ser	Lys	Ile	Ser	Gln	Gly	Gly	Leu	Gln	Arg	Ile		
			740					745					750				
Glu	Glu	Lys	Tyr	Thr	Trp	Lys	Leu	Tyr	Ser	Glu	Arg	Leu	Met	Thr	Leu		
	755						760					765					
Thr	Gly	Val	Tyr	Gly	Phe	Trp	Lys	Tyr	Val	Ser	Asn	Leu	Glu	Arg	Arg		
	770				775						780						
Glu	Thr	Arg	Arg	Tyr	Leu	Glu	Met	Leu	Tyr	Ala	Leu	Lys	Tyr	Arg	Thr		
785					790					795					800		
Met	Ala	Ser	Thr	Val	Pro	Leu	Ala	Val	Glu	Gly	Glu	Pro	Ser	Ser	Lys		
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<212> DNA

<213> Zea mays

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25

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gatgattggc ttgttcctgt cgttc

25

<210> 10

<211> 32

<212> DNA

<213> Zea mays

<400> 10

agagaagcca acgccawcgc ctcyatttcg tc

32

<210> 11

<211> 2757

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1) ... (2430)

<221> source

<222> (1) ... (39)

<223> Sorghum pronpinquum

<221> source

<222> (40)...(2757)

<223> Zea mays

<400> 11

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Met Ser Ala Pro Lys Leu Asn Arg Asn Ala Ser Ile Arg Asp Arg Val
   1               5               10               15

gag gac acc ctc cac gcg cac cgc aac gag ctc gtc gcc ctc ctc tcc   96
Glu Asp Thr Leu His Ala His Arg Asn Glu Leu Val Ala Leu Leu Ser
          20               25               30

aag tac gtg aac aag ggg aag ggc atc ctg cag ccg cac cac atc ctc  144
Lys Tyr Val Asn Lys Gly Lys Gly Ile Leu Gln Pro His His Ile Leu
          35               40               45

gac gcg ctc gac gag gtc cag ggc tcc ggg gtc cgc gcg ctc gcc gag  192
Asp Ala Leu Asp Glu Val Gln Gly Ser Gly Val Arg Ala Leu Ala Glu
          50               55               60

gga ccc ttc ctc gac gtc ctc cgc tcc gcg cag gag gcg atc gtg ctg  240
Gly Pro Phe Leu Asp Val Leu Arg Ser Ala Gln Glu Ala Ile Val Leu
          65               70               75               80

ccg ccg ttc gtg gcc atc gcg gtg cgc ccg cgc ccg gga gtt tgg gag  288
Pro Pro Phe Val Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu
          85               90               95
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tac gtc cgc gtc aac gtt cac gag ctc agc gtc gag cag ctc aca gtc 336

Tyr Val Arg Val Asn Val His Glu Leu Ser Val Glu Gln Leu Thr Val

100

105

110

tcg gag tac ctc cgc ttc aag gag gag ctt gtc gac ggc cag cac aat 384

Ser Glu Tyr Leu Arg Phe Lys Glu Glu Leu Val Asp Gly Gln His Asn

115

120

125

gat ccc tac gtt ctc gag ctt gac ttc gag ccg ttc aat gtc tca gtc 432

Asp Pro Tyr Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Val Ser Val

130

135

140

cca cgc cca aat cgg tca tca tct att gga aac ggt gtg cag ttc ctc 480

Pro Arg Pro Asn Arg Ser Ser Ser Ile Gly Asn Gly Val Gln Phe Leu

145

150

155

160

aac cga cac ttg tcc tca atc atg ttc cgc aac agg gat tgc ttg gag 528

Asn Arg His Leu Ser Ser Ile Met Phe Arg Asn Arg Asp Cys Leu Glu

165

170

175

ccc ctg ttg gat ttc ctc cgt ggc cac cgg cac aag ggg cat gtt atg 576

Pro Leu Leu Asp Phe Leu Arg Gly His Arg His Lys Gly His Val Met

180

185

190

atg ctt aat gat aga ata caa agc ttg ggg agg ctt cag tct gtg ctg 624

Met Leu Asn Asp Arg Ile Gln Ser Leu Gly Arg Leu Gln Ser Val Leu

195

200

205

acc aaa gct gag gag cac ttg tca aag ctc cct gct gac aca cca tac 672

Thr Lys Ala Glu Glu His Leu Ser Lys Leu Pro Ala Asp Thr Pro Tyr	
210	215
220	
tca caa ttt gct tat aaa ttt caa gag tgg ggc ctg gag aaa ggt tgg	720
Ser Gln Phe Ala Tyr Lys Phe Gln Glu Trp Gly Leu Glu Lys Gly Trp	
225	230
235	240
ggt gat aca gca gga cat gtt ttg gaa atg atc cat ctc ctt cta gac	768
Gly Asp Thr Ala Gly His Val Leu Glu Met Ile His Leu Leu Leu Asp	
245	250
255	
atc att cag gcg cca gac cca tct acc cta gag aaa ttc ttg ggg agg	816
Ile Ile Gln Ala Pro Asp Pro Ser Thr Leu Glu Lys Phe Leu Gly Arg	
260	265
270	
atc ccc atg att ttt aac gtt gtt gtg gta tcc cct cat gga tac ttt	864
Ile Pro Met Ile Phe Asn Val Val Val Val Ser Pro His Gly Tyr Phe	
275	280
285	
ggt caa gct aat gta tta ggc ttg cca gac aca gga gga cag atc gtc	912
Gly Gln Ala Asn Val Leu Gly Leu Pro Asp Thr Gly Gly Gln Ile Val	
290	295
300	
tat ata ctg gac caa gtc cgt gca cta gaa aat gag atg gtt ctc cgt	960
Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Val Leu Arg	
305	310
315	320
tta aag aaa caa ggg ctt gat gtt tcc cca aag att ctc att gtt act	1008
Leu Lys Lys Gln Gly Leu Asp Val Ser Pro Lys Ile Leu Ile Val Thr	

325	330	335	
cgg ctg ata cca gat gca aaa gga aca tca tgc aat cag cgg ctt gag			1056
Arg Leu Ile Pro Asp Ala Lys Gly Thr Ser Cys Asn Gln Arg Leu Glu			
340	345	350	
aga att agt gga aca cag cat act tac ata tta cga gtt ccc ttc aga			1104
Arg Ile Ser Gly Thr Gln His Thr Tyr Ile Leu Arg Val Pro Phe Arg			
355	360	365	
aat gaa aat ggg ata ctt aag aaa tgg ata tca aga ttt gat gtg tgg			1152
Asn Glu Asn Gly Ile Leu Lys Lys Trp Ile Ser Arg Phe Asp Val Trp			
370	375	380	
cca tat ctg gaa aca ttt gct gag gat gct gct ggt gaa att gct gct			1200
Pro Tyr Leu Glu Thr Phe Ala Glu Asp Ala Ala Gly Glu Ile Ala Ala			
385	390	395	400
gaa tta caa ggt act cca gac ttc ata att gga aac tac agt gat gga			1248
Glu Leu Gln Gly Thr Pro Asp Phe Ile Ile Gly Asn Tyr Ser Asp Gly			
405	410	415	
aat ctt gtg gcg tca ttg cta tct tac aag atg gga att acc cag tgc			1296
Asn Leu Val Ala Ser Leu Leu Ser Tyr Lys Met Gly Ile Thr Gln Cys			
420	425	430	
aac att gct cat gct ctg gaa aag act aag tat cca gat tca gac ata			1344
Asn Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp Ile			
435	440	445	

ttt tgg aag aat ttc gat gag aag tac cat ttc tcc tgc cag ttc act	1392
Phe Trp Lys Asn Phe Asp Glu Lys Tyr His Phe Ser Cys Gln Phe Thr	
450 455 460	
 gct gat ata att gct atg aac aat gct gat ttt atc atc acc agc aca	1440
Ala Asp Ile Ile Ala Met Asn Asn Ala Asp Phe Ile Ile Thr Ser Thr	
465 470 475 480	
 tac caa gaa att gct gga agc aaa aat act gtt gga cag tat gag agt	1488
Tyr Gln Glu Ile Ala Gly Ser Lys Asn Thr Val Gly Gln Tyr Glu Ser	
485 490 495	
 cat act gcc ttt act ctg cct ggt ctg tac cga gtt gtc cat ggg atc	1536
His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile	
500 505 510	
 gat gtc ttc gat cca aag ttc aat ata gtc tct cct gga gct gac atg	1584
Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met	
515 520 525	
 tcc ata tac ttt cca cat acc gag aag gcc aag cga ctc acc tct ctt	1632
Ser Ile Tyr Phe Pro His Thr Glu Lys Ala Lys Arg Leu Thr Ser Leu	
530 535 540	
 cat ggt tca atc gaa aat ttg att tat gac ccg gag caa aac gat gaa	1680
His Gly Ser Ile Glu Asn Leu Ile Tyr Asp Pro Glu Gln Asn Asp Glu	
545 550 555 560	

cac att ggg cat ctg gat gac cgg tca aag ccc atc ctc ttc tcc atg 1728
His Ile Gly His Leu Asp Asp Arg Ser Lys Pro Ile Leu Phe Ser Met

565 570 575

gca aga ctc gac agg gtg aag aac ata aca ggg ctg gtc gaa gct ttt 1776
Ala Arg Leu Asp Arg Val Lys Asn Ile Thr Gly Leu Val Glu Ala Phe

580 585 590

gct aag tgc gct aag ctg agg gag ctg gta aac ctt gtc gtc gtt gcc 1824
Ala Lys Cys Ala Lys Leu Arg Glu Leu Val Asn Leu Val Val Val Ala

595 600 605

ggg tac aat gat gtc aac aag tcc aag gac agg gaa gag atc gcg gag 1872
Gly Tyr Asn Asp Val Asn Lys Ser Lys Asp Arg Glu Glu Ile Ala Glu

610 615 620

ata gag aag atg cat gaa ctc atc aag acc cac aac ttg ttc ggg cag 1920
Ile Glu Lys Met His Glu Leu Ile Lys Thr His Asn Leu Phe Gly Gln

625 630 635 640

ttc cgc tgg atc tct gcc cag aca aac agg gcc cgt aac ggc gag ctc 1968
Phe Arg Trp Ile Ser Ala Gln Thr Asn Arg Ala Arg Asn Gly Glu Leu

645 650 655

tat cgc tac atc gct gat acc cat ggt gct ttc gta cag ccg gcc ttg 2016
Tyr Arg Tyr Ile Ala Asp Thr His Gly Ala Phe Val Gln Pro Ala Leu

660 665 670

tat gaa gcg ttc ggt ctc acc gtc gtt gag gcc atg acc tgt ggg ctt 2064

Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu	
675	680
685	
cct act ttc gcg acg ctc cat gga ggt cca gct gag atc ata gag cat	2112
Pro Thr Phe Ala Thr Leu His Gly Gly Pro Ala Glu Ile Ile Glu His	
690	695
700	
ggc gtc tcg ggc ttc cac att gac cgg tac cac ccc gaa cag gct gtt	2160
Gly Val Ser Gly Phe His Ile Asp Pro Tyr His Pro Glu Gln Ala Val	
705	710
715	720
aat ctg atg gcc gac ttc ttc gac cgg tgc aag caa gac cca gat cac	2208
Asn Leu Met Ala Asp Phe Phe Asp Arg Cys Lys Gln Asp Pro Asp His	
725	730
735	
tgg gtg aat ata tct gga gca ggg ctg cag cgc ata tac gag aag tac	2256
Trp Val Asn Ile Ser Gly Ala Gly Leu Gln Arg Ile Tyr Glu Lys Tyr	
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aca tgg aag ata tac tca gag agg ttg atg aca ctg gcc ggg gtc tac	2304
Thr Trp Lys Ile Tyr Ser Glu Arg Leu Met Thr Leu Ala Gly Val Tyr	
755	760
765	
ggc ttc tgg aag tac gtg tcg aag ctc gag agg ctg gag acg agg cgc	2352
Gly Phe Trp Lys Tyr Val Ser Lys Leu Glu Arg Leu Glu Thr Arg Arg	
770	775
780	
tac ctt gag atg ttc tac ata ctg aag ttc cgc gag ctg gcg aag acc	2400
Tyr Leu Glu Met Phe Tyr Ile Leu Lys Phe Arg Glu Leu Ala Lys Thr	

Pro Pro Phe Val Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu
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 Tyr Val Arg Val Asn Val His Glu Leu Ser Val Glu Gln Leu Thr Val
 100 105 110
 Ser Glu Tyr Leu Arg Phe Lys Glu Glu Leu Val Asp Gly Gln His Asn
 115 120 125
 Asp Pro Tyr Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Val Ser Val
 130 135 140
 Pro Arg Pro Asn Arg Ser Ser Ser Ile Gly Asn Gly Val Gln Phe Leu
 145 150 155 160
 Asn Arg His Leu Ser Ser Ile Met Phe Arg Asn Arg Asp Cys Leu Glu
 165 170 175
 Pro Leu Leu Asp Phe Leu Arg Gly His Arg His Lys Gly His Val Met
 180 185 190
 Met Leu Asn Asp Arg Ile Gln Ser Leu Gly Arg Leu Gln Ser Val Leu
 195 200 205
 Thr Lys Ala Glu Glu His Leu Ser Lys Leu Pro Ala Asp Thr Pro Tyr
 210 215 220
 Ser Gln Phe Ala Tyr Lys Phe Gln Glu Trp Gly Leu Glu Lys Gly Trp
 225 230 235 240
 Gly Asp Thr Ala Gly His Val Leu Glu Met Ile His Leu Leu Leu Asp
 245 250 255
 Ile Ile Gln Ala Pro Asp Pro Ser Thr Leu Glu Lys Phe Leu Gly Arg
 260 265 270
 Ile Pro Met Ile Phe Asn Val Val Val Val Ser Pro His Gly Tyr Phe
 275 280 285
 Gly Gln Ala Asn Val Leu Gly Leu Pro Asp Thr Gly Gly Gln Ile Val
 290 295 300
 Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Val Leu Arg

305	310	315	320
Leu Lys Lys Gln Gly Leu Asp Val Ser Pro Lys Ile Leu Ile Val Thr			
325	330	335	
Arg Leu Ile Pro Asp Ala Lys Gly Thr Ser Cys Asn Gln Arg Leu Glu			
340	345	350	
Arg Ile Ser Gly Thr Gln His Thr Tyr Ile Leu Arg Val Pro Phe Arg			
355	360	365	
Asn Glu Asn Gly Ile Leu Lys Lys Trp Ile Ser Arg Phe Asp Val Trp			
370	375	380	
Pro Tyr Leu Glu Thr Phe Ala Glu Asp Ala Ala Gly Glu Ile Ala Ala			
385	390	395	400
Glu Leu Gln Gly Thr Pro Asp Phe Ile Ile Gly Asn Tyr Ser Asp Gly			
405	410	415	
Asn Leu Val Ala Ser Leu Leu Ser Tyr Lys Met Gly Ile Thr Gln Cys			
420	425	430	
Asn Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp Ile			
435	440	445	
Phe Trp Lys Asn Phe Asp Glu Lys Tyr His Phe Ser Cys Gln Phe Thr			
450	455	460	
Ala Asp Ile Ile Ala Met Asn Asn Ala Asp Phe Ile Ile Thr Ser Thr			
465	470	475	480
Tyr Gln Glu Ile Ala Gly Ser Lys Asn Thr Val Gly Gln Tyr Glu Ser			
485	490	495	
His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile			
500	505	510	
Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met			
515	520	525	
Ser Ile Tyr Phe Pro His Thr Glu Lys Ala Lys Arg Leu Thr Ser Leu			
530	535	540	

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 Val Pro Leu Ala Ile Asp Gln Pro Gln
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